## **RAW SEQUENCE LISTING**

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Application Serial Number: [

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IFW16

RAW SEQUENCE LISTING DATE: 03/30/2005
PATENT APPLICATION: US/09/532,263A TIME: 10:35:32

Input Set : A:\10296A.sub.seq.txt

Output Set: N:\CRF4\03302005\I532263A.raw

## SEQUENCE LISTING

```
3 (1) GENERAL INFORMATION:
             (i) APPLICANT: Hilton, Douglas J.
      5
            (ii) TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR
      7
           (iii) NUMBER OF SEQUENCES: 25
      9
            (iv) CORRESPONDENCE ADDRESS:
     11
                   (A) ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
     13
                   (B) STREET: 400 Garden City Plaza
     14
                   (C) CITY: Garden City
     15
                   (D) STATE: New York
     16
                   (E) COUNTRY: United States of America
     17
                   (F) ZIP: 11530
     18
             (v) COMPUTER READABLE FORM:
     20
                   (A) MEDIUM TYPE: Floppy disk
     22
                   (B) COMPUTER: IBM PC compatible
     23
                   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     24
                   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     25
            (vi) CURRENT APPLICATION DATA:
     27
                   (A) APPLICATION NUMBER: US/09/532,263A
C--> 29
                   (B) FILING DATE: 22-Mar-2000
C--> 30
                   (C) CLASSIFICATION:
     31
          (viii) ATTORNEY/AGENT INFORMATION:
     33
                   (A) NAME: Presser, Leopold
     35
                   (B) REGISTRATION NUMBER: 19,827
     36
     37
                   (C) REFERENCE/DOCKET NUMBER: 10296
            (ix) TELECOMMUNICATION INFORMATION:
     39
                   (A) TELEPHONE: (516) 742-4343
     41
                   (B) TELEFAX: (516) 742-4366
     42
                   (C) TELEX: 203 901 SANS UR
     43
     45 (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
     47
     49
                   (A) LENGTH: 5 amino acids
                   (B) TYPE: amino acid
     50
                   (C) STRANDEDNESS: single
     51
     52
                   (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: DNA (genomic)
     54
     56
            (ix) FEATURE:
                   (A) NAME/KEY: misc_feature
     57
     58
                   (B) LOCATION: 3..3
                   (D) OTHER INFORMATION: /note= "Xaa at Position 3 is any amino acid"
     59
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     61
             Trp Ser Xaa Trp Ser
  -> 63
     64
```

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Input Set : A:\10296A.sub.seq.txt
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66 (2) INFORMATION FOR SEQ ID NO: 2:	
68 (i) SEQUENCE CHARACTERISTICS:	
70 (A) LENGTH: 1705 base pairs	
71 (B) TYPE: nucleic acid	
72 (C) STRANDEDNESS: single	
73 (D) TOPOLOGY: linear	
75 (ii) MOLECULE TYPE: DNA (genomic)	
77 (ix) FEATURE:	
79 (A) NAME/KEY: CDS	
80 (B) LOCATION: 451340	
82 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
84 GAGAGGGTGA GGGCGGAGGC CGCTGGCGGC GGCTGCCGCA GAAG ATG AGC AGC A	
85 Met Ser Ser S	er
86 1	
88 TGC TCA GGG CTG ACC AGG GTC CTG GTG GCC GTG GCT ACA GCC CTG GT	
89 Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala Thr Ala Leu Va	
90 5 10 15 2	
92 TCT TCC TCC TCC CCC TGC CCC CAA GCT TGG GGT CCT CCA GGG GTC CA	
93 Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val Gl	n
94 25 30 35	_
96 TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG TGC TGC CCC GGA GTG AG	
97 Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Se	r
98 40 45 50	
100 GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT GGA GAT TCA AGG CTG C	
101 Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu L	eu
102 55 60 65	<b>=</b> 0.00
104 CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA CTG GTC TTG GCC CAG G	
105 Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val Leu Ala Gln V	aı
106 70 75 80	ma 244
108 GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC CAG ACC CTG GAT GGT G	
109 Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly V	
110 05	.00
112 TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC TTT CCC CCA GCA CGT C	
113 Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro Pro Ala Arg P	10
114 105 110 115	GG 440
116 GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA AAC TTC TCC TGT ACT T	
117 Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe Ser Cys Thr T	гþ
118 120 125 130	'AC 488
120 AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC CGC TAC CTT ACT TCC T	
121 Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser T	Ϋ́
100	CC 536
124 AGG AAG AAG ACG CTG CCA GGA GCT GAG AGT CAG AGG GAA AGT CCA T	.cc 330
125 Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser Pro S	CI
126 150 155 160 128 ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT CTG GAG GCC TCC CGA T	'GT 584
128 ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT CTG GAG GCC TCC CGA T 129 Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg C	
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130 165 170 175 1 132 GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG TAC CGG ATC AAT GTG A	
132 GTG GTC CAT GGG GCA GAG TTC 1GG AGI GAG TAC CGG ATC AAT GTG A	
133 val val his Giy Ala Giu Fhe Tip Ser Giu Tyr Arg Tie Ash val I	111

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134					185					190					195		
															AGA		680
137	Glu	Val	Asn		Leu	Gly	Ala	Ser	Thr	Cys	Leu	Leu	Asp		Arg	Leu	
138				200					205					210			
															GAA		728
141	Gln	Ser	Ile	Leu	Arg	Pro	Asp	Pro	Pro	Gln	Gly	Leu		Val	Glu	Ser	
142			215					220					225				
															CCT		776
145	Val	Pro	Gly	Tyr	Pro	Arg	Arg	Leu	His	Ala	Ser	Trp	Thr	Tyr	Pro	Ala	
146		230					235					240					
															CAA		824
149	Ser	$\mathtt{Trp}$	Arg	Arg	Gln	Pro	His	Phe	Leu	Leu		Phe	Arg	Leu	Gln		
150						250					255					260	
															GGC		872
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															GTA		920
157	Glu	Glu	Val		Thr	Asp	Ala	Val		Gly	Leu	Pro	His		Val	Arg	
158				280					285					290			
															TGG		968
161	Val	Ser		Arg	Asp	Phe	Leu		Ala	Gly	Thr	Trp		Ala	Trp	Ser	
162			295					300					305	~	~~ ~		2016
															GAG		1016
165	Pro		Ala	Trp	Gly	Thr		ser	Thr	Gly	Pro		GIn	Asp	Glu	TTE	
166		310					315					320	~~-	a==	am.	aam	1064
															GTA		1064
		Asp	Trp	Ser	GIn	_	His	GLY	GIn	GIn		GIU	Ala	vaı	Val		
	325					330	~~	~~~		com	335	mma	a	aaa	an a	340	1112
															GAC		1112
	GIn	GIu	Asp	ser		Ala	Pro	Ата	Arg		ser	ьeu	GIII	PIO	Asp 355	PIO	
173	3.00	CC3	amm.	C 3 III	345	300	an a	aaa	mmc.	350	C 7 7	CITIZ	COT	стс		CCC	1160
															TTA Leu		1100
	Arg	PIO	Leu	360	нтв	Arg	Asp	PIO	365	GIU	GIII	vai	AIG	370	пец	ALG	
177	m/cm	OTTC	CCA		THE C	тст	TCC	СФФ		CTC	COT	ርጥጥ	GGA		CTG	GCA	1208
															Leu		2200
181	Ser	шец	375	116	FIIC	Der	Cys	380	CLY	alcu.	mu	• • • •	385				
	CTC	ccc		TCC	СТС	ACC	CTG		CGG	ΔGT	GGG	AAG		GGA	CCG	CAA	1256
															Pro		
185	пец	390	шси	112	шец	****9	395	9	••••		<b>U</b> -1	400		1		<del></del>	
	222		ccc	СТС	ጥጥር	GCA		ATG	ΔΤС	CCG	GTG		AAG	CTT	CCA	GGA	1304
																Gly	
	405	*-0	Q- <i>y</i>	204		410					415					420	
		CCA	AAC	CTG	CAG		ACC	CCA	GAG	AAC		AGC	TGA'	TTTC	ATC		1350
				Leu													
193					425	3				430							
	тст	AACC	CGG '	TCAG:		GG GG	GCAG	AAAG	A GG		GCAG	TGG	ATCC	CTG	TGGA	TGGAGG	1410
																CCGGCT	1470
																TACAGA	1530
	O. 11 11												_		-		

RAW SEQUENCE LISTING DATE: 03/30/2005
PATENT APPLICATION: US/09/532,263A TIME: 10:35:32

Input Set : A:\10296A.sub.seq.txt

Output Set: N:\CRF4\03302005\I532263A.raw

																CATGT GTGAA	1590 1650
205	GAGT	TGA	AT A	AAAA	GAGA	G G	AGTI	TTT	GAA	AAAA	AAA	AAA	AAAA	AA A	<b>LAAA</b>	1	1705
	(2)																
209	` '							STIC									
211		, ,		-				nino		ls							
212							no ac										
213							line										
215		(ii)	MOI														
217							_	N: S	SEQ I	D NO	): 3:	:					
	Met												Val	Ala	Val	Ala	
220	1				<sup>2</sup> 5		•			10					15		
		Ala	Leu	Val	Ser	Ser	Ser	Ser	Pro	Cys	Pro	Gln	Ala	Trp	Gly	Pro	
223				20					25	•				30	_		
	Pro	Glv	Val		Tvr	Glv	Gln	Pro	Gly	Arq	Pro	Val	Met	Leu	Cys	Cys	
226		1	35		- 2 -	2		40	•	_			45		-		
	Pro	Glv		Ser	Ala	Gly	Thr	Pro	Val	Ser	Trp	Phe	Arg	Asp	Gly	Asp	
229		50				•	55				-	60	_	_	_	_	
	Ser		Leu	Leu	Gln	Glv		qaA	Ser	Gly	Leu	Gly	His	Arg	Leu	Val	
232	65	5				70		-		-	75	-		_		80	
		Ala	Gln	Val	Asp	Ser	Pro	qaA	Glu	Gly	Thr	Tyr	Val	Cys	Gln	Thr	
235					85			-		90		-		_	95		
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238			•	100		•	•		105			_		110			
	Pro	Ala	Arq	Pro	Glu	Val	Ser	Cys	Gln	Ala	Val	Asp	Tyr	Glu	Asn	Phe	
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252	Ala	Ser	Arg	Cys	Val	Val	His	Gly	Ala	Glu	Phe	Trp	Ser	Glu	Tyr	Arg	
253			_	180					185					190			
255	Ile	Asn	Val	Thr	Glu	Val	Asn	Pro	Leu	Gly	Ala	Ser	Thr	Cys	Leu	Leu	
256			195					200					205				
258	Asp	Val	Arg	Leu	Gln	Ser	Ile	Leu	Arg	Pro	Asp	Pro	Pro	Gln	Gly	Leu	
259	-	210	Ū				215					220					
261	Arg	Val	Glu	Ser	Val	Pro	Gly	Tyr	Pro	Arg	Arg	Leu	His	Ala	Ser	Trp	
	225					230	_	_			235					240	
		Tyr	Pro	Ala	Ser	Trp	Arg	Arg	Gln	Pro	His	Phe	Leu	Leu	Lys	Phe	
265		•			245		_	_		250					255		
	Arq	Leu	Gln	Tyr	Arg	Pro	Ala	Gln	His	Pro	Ala	Trp	Ser	Thr	Val	Glu	
268	_			260	_				265					270			
	Pro	Ile	Gly	Leu	Glu	Glu	Val	Ile	Thr	Asp	Ala	Val	Ala	Gly	Leu	Pro	
271			275					280		-			285				
	His	Ala	Val	Arg	Val	Ser	Ala	Arg	Asp	Phe	Leu	Asp	Ala	Gly	Thr	Trp	
274		290		_			295	_	_			300					
		Ala	Trp	Ser	Pro	Glu	Ala	Trp	Gly	Thr	Pro	Ser	Thr	Gly	Pro	Leu	
			-					_	_								

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277						310					315					320	
279	Gln	Asp	Glu	Ile	Pro	Asp	Trp	Ser	Gln	Gly	His	Gly	Gln	Gln	Leu	Glu	
280					325					330					335		
282	Ala	Val	Val	Ala	Gln	Glu	Asp	Ser	Pro	Ala	Pro	Ala	Arg	Pro	Ser	Leu	
283				340			_		345					350			
	Gln	Pro	Asp		Ara	Pro	Leu	Asp	His	Ara	Asp	Pro	Leu	Glu	Gln	Val	
286			355		5			360			-		365				
	בות	Val		Δla	Ser	Len	Glv		Phe	Ser	Cvs	Leu		Leu	Ala	Val	
289	AIG	370	шси	niu	DCI	<b>D</b> Cu	375				0,10	380	1				
	C111		Len	λl =	T.011	Gl v		Trn	T.e.11	Δra	T.e11		Ara	Ser	Glv	Lvs	
		Ата	пец	AIG	шеu	390	шеи	115	шси	9	395	••••	-, 9		U-1	400	
292		C1.,	Dro	Cln	Two		Glv	T.011	T.211	Δla		Met	Tle	Pro	Val		
	Asp	GIY	PIO	GIII	405	PIO	GIY	шец	пец	410	110	ricc	110	110	415	O.L.	
295	•	<b>7</b>	D	<b>01</b>		Deco	7 ~~	T 011	C1 5		Thr	Dro	Clu	λan		Ser	
	гуѕ	Leu	Pro	_	тте	PIO	ASII	neu		Arg	1111	PIO	Gru	Asn	FIIE	261	
298	4 - 1			420					425					430			
	(2)						ID 1										
303		(i)	-	-			CTER										
305			-	•			300 k		_	rs							
306							leic										
307			((	c) s:	rani	DEDNI	ESS:	sing	gle								,
308			(1	) T(	OPOL	OGY:	line	ear									
310		(ii)	MOI	LECUI	JE T	YPE:	CDN	A									
312		(iii)	HY!	POTHI	ETIC	AL: 1	10										
314		(iv)	AN'	ri-si	ENSE	: NO											
210		12			_												
317		(lx	) FE	ATURI	3:												
317		(1X			E: AME/1	KEY:	CDS										
		(1X)	(2	A) N	AME/1		CDS	139	96								
319			() (1	A) NA B) LO	AME/I	ION:				ID NO	D: 4	:					
319 320 322		(xi)	() (1 SE(	A) NA B) LO QUENO	AME/I OCAT: CE DI	ION: ESCR	128. PTIC	ON: S	SEQ :				GAAG	CCT (	CAGT'	rttgga	60
319 320 322 324	TCT	(xi)	() (1) SE( GCC (	A) NA B) LO QUENO TTACO	AME/I OCAT: CE DI CCCA(	ION: ESCRI CT TO	128 PTIC GTGC	ON: S	SEQ :	TTTT(	CTCC	TAG				TTTGGA CCTCTC	60 120
319 320 322 324 326	TCT/	(xi) AACAG	() (1) SEC C CSE AGC (	A) NA B) L( QUEN( CTAC( CAGG(	AME/I OCAT: CE DI CCCA( CTTT)	ION: ESCRI CT TO AG CI	128 PTIC GGTGC	ON: S CATCI ATCT(	SEQ : A AT' C AGO	TTTT( GGGT(	CTCC CGGG	TAGG GAT	TTTT(	GAC '	rcta(	CCTCTC	
319 320 322 324 326 328	TCT/	(xi) AACAG	() (1) () SE( () SGC () ATG	A) NA B) LO QUENO TTACO CAGGO AGC	AME/I DCAT: CE DI CCCAC CTTTI AGC	ION: ESCR: CT TO AG C' AGC	128 PTIC GGTGC FCCC TGC	ON: S CATCI ATCTO TCA	SEQ : A AT' C AGG GGG	TTTT( GGGT( CTG	CTCC CGGG AGC	TAGO GAT' AGG	TTTTC GTC	GAC '	CTA GTG	CCTCTC GCC	120
319 320 322 324 326 328 329	TCT/	(xi) AACAG	() () SE( SCC ) AGC ( ATG Met	A) NA B) LO QUENO TTACO CAGGO AGC	AME/I DCAT: CE DI CCCAC CTTTI AGC	ION: ESCR: CT TO AG C' AGC	128 IPTIC GTGC ICCC TGC Cys	ON: S CATCI ATCTO TCA	SEQ : A AT' C AGG GGG	TTTT( GGGT( CTG	CTCC CGGG AGC	TAGO GAT' AGG	TTTTC GTC	GAC '	CTA GTG	CCTCTC GCC	120
319 320 322 324 326 328 329 330	TCTA GAGG CCCA	(xi) AACAG GAAGA	() (1) SE() SCC () AGC () ATG Met 1	A) NA B) LO QUENO CTACO CAGGO AGC Ser	AME/I DCAT: CE DI CCCAC CTTTI AGC Ser	ION: ESCRI CT TO AG CI AGC Ser	128 PTIC GGTGC TCCC TGC Cys 5	ON: S CATCA ATCTO TCA Ser	SEQ TANGE AGG GGG Gly	TTTT( GGGT( CTG Leu	CTCC CGGG AGC Ser	TAGG GATT AGG Arg 10	GTC Val	GAC ' CTG Leu	GTG Val	CCTCTC GCC Ala	120
319 320 322 324 326 328 329 330 332	TCTA GAGG CCCA	(xi) AACAG BAAGA ACAG	() (1) SE() SGC () AGC () ATG Met 1 ACA	A) NA B) LO QUENO CAGGO AGC Ser	AME/I DCAT: DE DI DCCAC CTTTA AGC Ser CTG	ION: ESCRI CT TO AG CT AGC Ser GTG	128 IPTIO GGTGO TGC TGC Cys 5 TCT	ON: S CATCA TCA TCA Ser	EEQ TA ATT	TTTT( GGGT( CTG Leu TCC	CTCC CGGG AGC Ser	TAGO GATT AGG Arg 10 TGC	GTC Val CCC	GAC CTG Leu CAG	CTA GTG Val GCC	CCTCTC GCC Ala TGG	120 169
319 320 322 324 326 328 329 330 332 333	TCTA GAGG CCCA ; GTG Val	(xi) AACAG BAAGA ACAG	() (1) SE() SGC () AGC () ATG Met 1 ACA	A) NA B) LO QUENO CAGGO AGC Ser	AME/I DCAT: DE DI DCCAC CTTTA AGC Ser CTG	ION: ESCRI CT TO AG CT AGC Ser GTG Val	128 IPTIO GGTGO TGC TGC Cys 5 TCT	ON: S CATCA TCA TCA Ser	EEQ TA ATT	TTTT( GGGT( CTG Leu TCC	CTCC CGGG AGC Ser CCC Pro	TAGO GATT AGG Arg 10 TGC	GTC Val CCC	GAC ' CTG Leu	CTA GTG Val GCC	CCTCTC GCC Ala TGG	120 169
319 320 322 324 326 328 329 330 332 333 334	TCTZ GAGG CCCZ GTG Val 15	(xi) AACAG AACAG ACAG GCT Ala	() (1) () SE() GCC () AGC () ATG Met 1 ACA Thr	A) NA B) LO QUENO TTACO CAGGO AGC Ser GCC Ala	AME/I DCAT: CE DI CCCAC CTTTI AGC Ser CTG Leu	ION: ESCRI CT TO AG CT AGC Ser GTG Val 20	128 IPTIC GGTGC TGC Cys 5 TCT Ser	ON: S CATCI ATCTO TCA Ser GCC Ala	EEQ AATTO AGG GGG Gly TCC Ser	TTTTO GGGTO CTG Leu TCC Ser	CTCC CGGG AGC Ser CCC Pro 25	TAGG GATT AGG Arg 10 TGC Cys	GTC Val CCC Pro	GAC CTG Leu CAG Gln	CTAC GTG Val GCC Ala	GCTCTC GCC Ala TGG Trp 30	120 169 217
319 320 322 324 326 328 329 330 332 333 334 336	TCTZ GAGG CCCZ GTG Val 15 GGC	(xi) AACAG GAAGA ACAG GCT Ala	() (1) SE() GCC 'AGC () ATG Met 1 ACA Thr	A) NA B) LO QUENO TTACO CAGGO AGC Ser GCC Ala	AME/IDCAT: CE DI CCCAC CTTTI AGC Ser CTG Leu GTC	ION: ESCRI TO AG CO AGC Ser GTG Val 20 CAG	128 IPTIC GGTGO TGC Cys 5 TCT Ser	ON: SCATCA TCA TCA Ser GCC Ala GGG	EEQ A ATTO AGG GGG Gly TCC Ser	TTTTC GGGTC CTG Leu TCC Ser	CTCC CGGG AGC Ser CCC Pro 25 GGC	TAGG GATT AGG Arg 10 TGC Cys	GTC Val CCC Pro	GAC CTG Leu CAG Gln GTG	CTAC GTG Val GCC Ala	CCTCTC GCC Ala TGG Trp 30 CTG	120 169
319 320 322 324 326 328 329 330 332 333 334 336 337	TCTZ GAGG CCCZ GTG Val 15 GGC	(xi) AACAG GAAGA ACAG GCT Ala	() (1) SE() GCC 'AGC () ATG Met 1 ACA Thr	A) NA B) LO QUENO TTACO CAGGO AGC Ser GCC Ala	AME/IDCAT: CE DICCCAC CTTTI AGC Ser CTG Leu GTC Val	ION: ESCRI TO AG CO AGC Ser GTG Val 20 CAG	128 IPTIC GGTGO TGC Cys 5 TCT Ser	ON: SCATCA TCA TCA Ser GCC Ala GGG	EEQ A ATTO AGG GGG Gly TCC Ser	TTTTC GGGTC CTG Leu TCC Ser CCA Pro	CTCC CGGG AGC Ser CCC Pro 25 GGC	TAGG GATT AGG Arg 10 TGC Cys	GTC Val CCC Pro	GAC CTG Leu CAG Gln	GTG Val GCC Ala AAG Lys	CCTCTC GCC Ala TGG Trp 30 CTG	120 169 217
319 320 322 324 326 328 329 330 332 333 334 336 337 338	TCTA GAGG CCCA GTG Val 15 GGC Gly	(xi) AACAG BAAGG ACAG GCT Ala CCC Pro	() (1) SEC GCC () AGC () ATG Met 1 ACA Thr CCA	A) NA B) LO QUENO CAGGO AGC Ser GCC Ala GGG Gly	AME/IDCAT: DCCAC CTTTI AGC Ser CTG Leu GTC Val 35	ION: ESCRI AG CT AGC Ser GTG Val 20 CAG Gln	128 IPTIC GGTGC TGC Cys 5 TCT Ser TAT	ON: S CATCA TCA Ser GCC Ala GGG Gly	SEQ TARGET AGE	TTTTC CTG Leu TCC Ser CCA Pro 40	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly	TAGG GAT AGG Arg 10 TGC Cys AGG Arg	GTC Val CCC Pro TCC Ser	CTG Leu CAG Gln GTG Val	GTG Val GCC Ala AAG Lys 45	TGG Trp 30 CTG Leu	120 169 217 265
319 320 322 324 326 328 329 330 332 333 334 336 337 338 340	TCTAGAGGCCCA	(xi) AACAG GAAGA ACAG GCT Ala CCC Pro	(I) SEC	A) NA B) LO QUENO CAGGO AGC Ser GCC Ala GGG GGA	AME/IDCAT: DCAT: DCCAC CTTTA AGC Ser CTG Leu GTC Val 35 GTG	ION: ESCRI TT TO AG CT AGC Ser GTG Val 20 CAG Gln ACT	128 IPTIC GGTGC TGC Cys 5 TCT Ser TAT Tyr	ON: SCATCE ATCTO TCA Ser GCC Ala GGG Gly GGG	A ATT A AGG GGG Gly TCC Ser CAG Gln	TTTTC CTG Leu TCC Ser CCA Pro 40 CCA	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly	TAGG GATT AGG Arg 10 TGC Cys AGG Arg	GTC Val CCC Pro TCC Ser	CTG Leu CAG Gln GTG Val	GTG Val GCC Ala AAG Lys 45 CGG	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT	120 169 217
319 320 324 326 328 329 330 332 333 334 336 337 338 340 341	TCTAGAGGCCCA	(xi) AACAG GAAGA ACAG GCT Ala CCC Pro	(I) SEC	A) NA B) LO QUENO TTACO CAGGO AGC Ser GCC Ala GGG Gly GGA GIY	AME/IDCAT: DCAT: DCCAC CTTTA AGC Ser CTG Leu GTC Val 35 GTG	ION: ESCRI TT TO AG CT AGC Ser GTG Val 20 CAG Gln ACT	128 IPTIC GGTGC TGC Cys 5 TCT Ser TAT Tyr	ON: SCATCE ATCTO TCA Ser GCC Ala GGG Gly GGG	A ATT C AGG GGG Gly TCC Ser CAG Gln GAC Asp	TTTTC CTG Leu TCC Ser CCA Pro 40 CCA	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly	TAGG GATT AGG Arg 10 TGC Cys AGG Arg	GTC Val CCC Pro TCC Ser	CTG Leu CAG Gln GTG Val TTT Phe	GTG Val GCC Ala AAG Lys 45 CGG	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT	120 169 217 265
319 320 322 324 326 328 329 330 332 333 334 336 337 338 340 341 342	TCTAGAGGCCCCAGGGCGCGCGCGCGCGCGCGCGCGCGCG	(xi) AACAG GAAGA ACAG GCT Ala CCC Pro TGT Cys	(I) SEC SCC SAGC (ATG ATG ACA Thr CCA Pro	A) NA B) LO QUENO CAGGO AGC Ser GCC Ala GGG Gly GGA Gly	AME/IDCAT: DCCAC CTTTA AGC Ser CTG Leu GTC Val 35 GTG Val	ION: ESCRI TT TO AG CT AGC Ser GTG Val 20 CAG Gln ACT Thr	128 IPTIC GGTGC TGC Cys 5 TCT Ser TAT Tyr GCC Ala	ON: SEATCH ATCTO TCA Ser GCC Ala GGG Gly GGG Gly	EEQ CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TTTTC GGGTC CTG Leu TCC Ser CCA Pro 40 CCA Pro	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val	TAGG GATT AGG Arg 10 TGC Cys AGG Arg TCC Ser	GTC Val CCC Pro TCC Ser TGG Trp	CAG Gln GTG Val TTT Phe 60	GTAG GTG Val GCC Ala AAG Lys 45 CGG Arg	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp	120 169 217 265 313
319 320 322 324 326 328 329 330 332 333 334 336 337 338 340 341 342 344	TCTA GAGG CCCA GTG Val 15 GGC Gly TGT Cys	(xi) AACAG GAAGA ACAG GCT Ala CCC Pro TGT Cys	(I) SE(GCC CACCACCACCACCACCACCACCACCACCACCACCACC	A) NA B) LO QUENO TTACO CAGGO AGC Ser GCC Ala GGG Gly GGA Gly 50 AAG	AME/IDCAT: DCCAC CTTTA AGC Ser CTG Leu GTC Val 35 GTG Val CTG	ION: ESCRI TTO AG CT AGC Ser GTG Val 20 CAG Gln ACT Thr	128 IPTIC GGTGC TGC Cys 5 TCT Ser TAT Tyr GCC Ala	ON: SEATCH ATCTO TCA SET GCC Ala GGG Gly GGG Gly GGA	EEQ SEQ SEQ ATT CO SET CAG Gln GAC Asp 55 CCT	TTTTC GGGTC CTG Leu TCC Ser CCA Pro 40 CCA Pro	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val	TAGG GATT AGG Arg 10 TGC Cys AGG Arg TCC ser	TTTTC GTC Val CCC Pro TCC Ser TGG Trp CTA	CAG Gln GTG Val TTT Phe 60 GGG	GCTAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp	120 169 217 265
319 320 324 326 328 329 330 332 333 334 336 337 338 340 341 342 344 345	TCTA GAGG CCCA GTG Val 15 GGC Gly TGT Cys	(xi) AACAG GAAGA ACAG GCT Ala CCC Pro TGT Cys	(I) SE(GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	A) NA B) LO QUENO TTACO CAGGO AGC Ser GCC Ala GGG Gly GGA Gly 50 AAG	AME/IDCAT: DCCAC CTTTA AGC Ser CTG Leu GTC Val 35 GTG Val CTG	ION: ESCRI TTO AG CT AGC Ser GTG Val 20 CAG Gln ACT Thr	128 IPTIC GGTGC TGC Cys 5 TCT Ser TAT Tyr GCC Ala	ON: SEATCH ATCTO TCA SET GCC Ala GGG Gly GGG Gly GGA GGY GGA GGY	EEQ SEQ SEQ ATT CO SET CAG Gln GAC Asp 55 CCT	TTTTC GGGTC CTG Leu TCC Ser CCA Pro 40 CCA Pro	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val	TAGG GATT AGG Arg 10 TGC Cys AGG Arg TCC ser	TTTTC GTC Val CCC Pro TCC Ser TGG Trp CTA Leu	CAG Gln GTG Val TTT Phe 60	GCTAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp	120 169 217 265 313
319 320 324 326 328 329 330 332 333 334 336 337 338 340 341 342 344 345 346	TCTA GAGG CCCA GTG Val 15 GGC Gly TGT Cys	(xi) AACAG GAAGA ACAG GCT Ala CCC Pro TGT Cys GAG Glu	(I) SE(GCC CACACACACACACACACACACACACACACACACACA	A) NA B) LO QUENO TTACO CAGGO AGC Ser GCC Ala GGG Gly GGA Gly 50 AAG Lys	AME/IDCAT: DCCAC CTTTI AGC Ser CTG Leu GTC Val 35 GTG Val CTG Leu	ION: ESCRI TO AG CT AGC Ser GTG Val 20 CAG Gln ACT Thr	128 IPTIC GGTGC TGC Cys 5 TCT Ser TAT Tyr GCC Ala CAG	ON: SEATCH ATCTO TCA Ser GCC Ala GGG Gly GGA Gly 70	GEQ CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TTTTC GGGTC CTG Leu TCC Ser CCA Pro CCA Pro GAC Asp	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val	TAGG GATTAGG Arg 10 TGC Cys AGG Arg TCC Ser GGG Gly	TTTTC GTC Val CCC Pro TCC Ser TGG Trp CTA Leu 75	CAG Gln GTG Val TTT Phe 60 GGG Gly	GCTAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TGG Trp 30 CTG Leu GAT Asp GAA Glu	120 169 217 265 313 361
319 320 324 326 328 329 330 332 333 334 336 337 338 340 341 342 344 345 346 348	TCTAGAGG CCCA GTG Val 15 GGC Gly TGT Cys GGG Gly	(xi) AACAG GAAGA ACAG GCT Ala CCC Pro TGT Cys GAG Glu	(I) SE(GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	A) NA B) LO QUENO TTACO CAGGO AGC Ser GCC Ala GGG Gly 50 AAG Lys	AME/IDCAT: DCAT: DCCAC CTTTI AGC Ser CTG Leu GTC Val 35 GTG Val CTG Leu CTG	ION: ESCR: CT TO AG CT AGC Ser GTG Val 20 CAG Gln ACT Thr CTC Leu GCA	128 IPTIC GGTGC TGC Cys 5 TCT Ser TAT Tyr GCC Ala CAG Gln	ON: SEATCH TCA SET GCC Ala GGG Gly GGA GGLY 70 AGC	GEQ CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TTTTCGGGTCCTGGTCCCACCCACCCACCCACCCACCCAC	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val TCT Ser	TAGG GATT AGG Arg 10 TGC Cys AGG Arg TCC Ser GGG Gly	TTTTC GTC Val CCC Pro TCC Ser TGG Trp CTA Leu 75 ACC	CAG Gln GTG Val TTT Phe 60 GGG Gly	GCC Ala AAG Lys 45 CGG Arg CAT His	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp GAA Glu TGC	120 169 217 265 313
319 320 324 326 328 329 330 332 333 334 336 337 348 341 342 344 345 346 348 349	TCTAGAGG CCCA GTG Val 15 GGC Gly TGT Cys GGG Gly	(xi) AACAG GAAGA ACAG GCT Ala CCC Pro TGT Cys GAG Glu GTC Val	(I) SE(GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	A) NA B) LO QUENO TTACO CAGGO AGC Ser GCC Ala GGG Gly 50 AAG Lys	AME/IDCAT: DCAT: DCCAC CTTTI AGC Ser CTG Leu GTC Val 35 GTG Val CTG Leu CTG	ION: ESCR: CT TO AG CT AGC Ser GTG Val 20 CAG Gln ACT Thr CTC Leu GCA	128 IPTIC IPTIC ITGC Cys 5 TCT Ser TAT Tyr GCC Ala CAG Gln GAC Asp	ON: SEATCH TCA SET GCC Ala GGG Gly GGA GGLY 70 AGC	GEQ CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TTTTCGGGTCCTGGTCCCACCCACCCACCCACCCACCCAC	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val TCT Ser	TAGG GATTAGG Arg 10 TGC Cys AGG Arg TCC ser GGG Gly	TTTTC GTC Val CCC Pro TCC Ser TGG Trp CTA Leu 75 ACC	CAG Gln GTG Val TTT Phe 60 GGG Gly	GCC Ala AAG Lys 45 CGG Arg CAT His	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp GAA Glu TGC	120 169 217 265 313 361
319 320 324 326 328 329 330 332 333 334 336 337 338 340 341 342 344 345 346 348 349 350	TCTAGAGGCCCCATAGGCCGTGTGTCTGTCTGTCTGTCTG	(xi) AACAG GAAGA ACAG GCT Ala CCC Pro TGT Cys GAG Glu GTC Val	(I) SE(GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GCC Ala GGA Gly SO AAG Lys GCC Ala	AME/IDCAT: DCAT: DCCAC CCTTTI AGC Ser CTG Leu GTC Val GTG Val CTG Leu CAG Gln	ION: ESCR: CT TO AG CT AGC Ser GTG Val 20 CAG Gln ACT Thr CTC Leu GCA Ala	128 IPTIC GGTGC TGC Cys 5 TCT Ser TAT Tyr GCC Ala CAG Gln GAC Asp	ON: SEATCH TCA SET GCC Ala GGG Gly GGA Gly 70 AGC SET	GEQ CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TTTTCGGGTCGCTGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val TCT Ser GAG Glu	TAGG GATTAGG Arg 10 TGC Cys AGG Arg TCC Ser GGG Gly GGC Gly	CCC Pro TCC Ser TGG Trp CTA Leu 75 ACC	CAG Gln GTG Val TTT Phe 60 GGG Gly TAC	GCC Ala AAG Lys 45 CGG Arg CAT His	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp GAA Glu TGC Cys	120 169 217 265 313 361 409
319 320 324 326 328 329 330 332 333 334 336 337 338 340 341 342 344 345 346 348 349 350	TCTAGAGGCCCCATAGGCCGTGTGTCTGTCTGTCTGTCTG	(xi) AACAG GAAGA ACAG GCT Ala CCC Pro TGT Cys GAG Glu GTC Val	(I) SE(GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GCC Ala GGA Gly SO AAG Lys GCC Ala	AME/IDCAT: DCAT: DCCAC CCTTTI AGC Ser CTG Leu GTC Val GTG Val CTG Leu CAG Gln	ION: ESCR: CT TO AG CT AGC Ser GTG Val 20 CAG Gln ACT Thr CTC Leu GCA Ala	128 IPTIC GGTGC TGC Cys 5 TCT Ser TAT Tyr GCC Ala CAG Gln GAC Asp	ON: SEATCH TCA SET GCC Ala GGG Gly GGA Gly 70 AGC SET	GEQ CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TTTTCGGGTCGCTGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val TCT Ser GAG Glu	TAGG GATTAGG Arg 10 TGC Cys AGG Arg TCC Ser GGG Gly GGC Gly	CCC Pro TCC Ser TGG Trp CTA Leu 75 ACC	CAG Gln GTG Val TTT Phe 60 GGG Gly TAC	GCC Ala AAG Lys 45 CGG Arg CAT His	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp GAA Glu TGC	120 169 217 265 313 361

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/30/2005 PATENT APPLICATION: US/09/532,263A TIME: 10:35:33

Input Set : A:\10296A.sub.seq.txt

Output Set: N:\CRF4\03302005\1532263A.raw

## Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos.3 \( \)
Seq#:8; N Pos. 7
Seq#:9; N Pos. 7
Seq#:23; N Pos. 7

## VERIFICATION SUMMARY

DATE: 03/30/2005

PATENT APPLICATION: US/09/532,263A

TIME: 10:35:33

Input Set : A:\10296A.sub.seq.txt

Output Set: N:\CRF4\03302005\I532263A.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0